

	1		50
EG327	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVATAVLA TLLFATVQAS.
BZ198	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLFATVQAN
BZ10	MNKISRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLFATVQAN
H15	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLFATVQAN
EG329	MNEILRIIWN	SALNAWVVVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAS
PMC21	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAS
H38	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAN
P20	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA SATVATAVLA TLLSATVQAN
Z2491	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAN
H41	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA SATVKTAVLA TLLFATVQAN
Consensus	<u>MN-I-RIIWN</u>	<u>SALNAWV-VS</u>	<u>ELTRNHTKRA SATV-TAVLA TLL-ATVQA-</u>

C1

	51		100
EG327	TTDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.VTED SNWGVYFDKK
BZ198	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
BZ10	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
H15	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG TGEKE.GTED SNWAVYFDEK
EG329	ANNEEQEEDL	YLDPVLRIVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
PMC21	ANNEEQEEDL	YLDPVQRTVA	VLIVNSDKEG TGEKEKVEEN SDWAVYFNEK
H38	ATDED...EEE	ELEPVRSAL	VLQFMIDKEG NGENE.STGN IGWSIYYDNH
P20	ATDTD...EDE	ELESVARSAL	VLQFMIDKEG NGEIESTGDI GWSIYYDDHN
Z2491	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SGELET...I SLSMTNDSKE
H41	ATDED...EEE	ELESVQR.SV	VGSIQASMEG SVELET...I SLSMTNDSKE
Consensus	-----	-L--V-R--	V-----EG --E-E-----

V1

	101		150
EG327	GVLTAGTITL	KAGDNLKIKQ	NTNENTNASSFTYSLK KDLTDLTSVG
BZ198	RVLKAGAITL	KAGDNLKIKQ	NTNENTNDSSFTYSLK KDLTDLTSVE
BZ10	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT NDSSEFTYSLK KDLTDLTSVE
H15	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT NDSSEFTYSLK KDLTDLTSVE
EG329	GVLTAAREITL	KAGDNLKIKQ	NG...TN...FTYSLK KDLTDLTSVG
PMC21	GVLTAAREITL	KAGDNLKIKQ	NG...TN...FTYSLK KDLTDLTSVG
H38	NTLHGATVTL	KAGDNLKIKQ	NTNKNTNENT NDSSEFTYSLK KDLTDLTSVE
P20	TLHG.ATVTL	KAGDNLKIKQ	SGKD.....FTYSLK KELKDLTSVE
Z2491	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASSFTYSLK KDLTGLINVE
H41	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASSFTYSLK KDLTGLINVE
Consensus	-----TL	<u>KAGDNLKIKQ</u>	-----FTYSLK <u>K-L--L--V-</u>
	V1	C2	V2 C3

	151		200
EG327	TEKLSFSANS	NKVNITSDTK	GLNFAKKTAE TNGDPTVHLN GIGSTLTDTL
BZ198	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
BZ10	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H15	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
EG329	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
PMC21	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H38	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
P20	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
Z2491	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDTL
H41	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG TNGDPTVHLN GIGSTLTDML
Consensus	<u>TEKLSF-AN-</u>	<u>-KVNI-SDTK</u>	<u>GLNFAK-TA- TNGD-TVHLN GIGSTLTD-I</u>

C3

FIG. 1

	201		250
EG327	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVKP GTTAS..DNV
BZ198	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVKP GTTAS..DNV
BZ10	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVKP GTTAS..DNV
H15	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVKP GTTAS..DNV
EG329	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVKP GTTAS..DNV
PMC21	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVKP GTTAS..DNV
H38	LNTGATTNVT	NDNVTDDKKK	RAASVKDVLN AGWNIKGVKP GTTAS..DNV
P20	AGSSASHVDA	GNQST..HYT	RAASIKDVLN AGWNIKGVKP GSTTGQSENV
Z2491	AGSSASHVDA	GNQST..HYT	RAASIKDVLN AGWNIKGVKP GSTTGQSENV
H41	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN AGWNIKGVKP GTTAS..DNV
Consensus	----A-----	----T-----	RAAS-KDVLN AGWNIKGVK- G-T-----NV
	V3		C4 V4

	251		300
EG327	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
H15	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGL
H38	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
P20	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK RTEVKIGAKT SVIKEKDGL
H41	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK KTEVKIGAKT SVIKEKDGL
Consensus	DFV-TYDTVE	FLSADTKTTT	VNVESKDNGK -TEVKIGAKT SVIKEKDGL
			C5

	301		350
EG327	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
BZ198	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
BZ10	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
H15	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
EG329	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
PMC21	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
H38	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
P20	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
Z2491	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
H41	VTGKDKGEND	SSTDKEGGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
Consensus	VTGK-K-EN-	SSTD-GEGLV	TAKEVIDAVN KAGWRMKT TT ANGQTGQADK
			C5

	351		400
EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN TVMYDVNVGD ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN TVKYDVNVGD ALNVNQLQNS
BZ10	FETVTSGTKV	TFASNGTTA	TVSKDDQGN TVKYDVNVGD ALNVNQLQNS
H15	FETVTSGTKV	TFASNGTTA	TVSKDDQGN TVKYDVNVGD ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN TVMYDVNVGD ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN TVMYDVNVGD ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN TVKYDVNVGD ALNVNQLQNS
P20	FETVTSGTKV	TFASNGTTA	TVSKDDQGN TVKYDVNVGD ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGN TVMYDVNVGD ALNVNQLQNS
H41	FETVTSGTKV	TFASNGTTA	TVSKDDQGN TVKYDVNVGD ALNVNQLQNS
Consensus	FETVTSGT-V	TFASG-GTTA	TVSKDDQGN TV-YDVNVGD ALNVNQLQNS
			C5

FIG. 1 cont.

401 450

EG327	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
BZ198	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
BZ10	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
H15	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
EG329	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
PMC21	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
H38	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
P20	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
Z2491	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EISRNGKNID
H41	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE	TVNINAGNNI	EITRNGKNID
Consensus	<u>GWNLDSKAVA</u>	<u>GSSGKVISGN</u>	<u>VSPSKGKMDE</u>	<u>TVNINAGNNI</u>	<u>EI-RNGKNID</u>

C5

451 500

EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
BZ198	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDTNK	PVRITNVAPG
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA	LNVGSKKDNK	PVRITNVAPG
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKGA	LNVGSKDANK	PVRITNVAPG
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Z2491	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA	LNVGSKDANK	PVRITNVAPG
Consensus	<u>IATSM-PQFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---A</u>	<u>LNVGSK--NK</u>	<u>PVRITNVAPG</u>

C5

501 550

EG327	VKEGDVTNVA	QLKGVAQNIN	NHIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ198	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
BZ10	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
H15	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLAQAYLPG
EG329	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
PMC21	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H38	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
P20	VKEGDVTNVA	QLKGVAQNIN	NRIDNVNGNA	RAGIAQAIAT	AGLAQAYLPG
Z2491	VKEGDVTNVA	QLKGVAQNIN	NRIDNVDGNA	RAGIAQAIAT	AGLVQAYLPG
H41	VKEGDVTNVA	QLKGVAQNIN	NRIDNVNGNA	RAGIAQAIAT	AGLVQAYLPG
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNIN</u>	<u>N-IDNV-GNA</u>	<u>RAGIAQAIAT</u>	<u>AGL-QAYLPG</u>

C5

551 600

EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ198	KSMMAIGGDT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGASASV
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW	VIKGTASGNS	RGHFGTSASV
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW	IIKGTASGNS	RGHFGASASV
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW	IIKGTASGNS	RGHFGASASV
Consensus	<u>KSMMAIGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW</u>	<u>-IKGTASGNS</u>	<u>RGHFG-SASV</u>

C5

FIG. 1 cont.

601
EG327 GYQW.
BZ198 GYQW.
BZ10 GYQW.
H15 GYQW.
EG329 GYQW.
PMC21 GYQW.
H38 GYQW.
P20 GYQW.
Z2491 GYQW.
H41 GYQW.
Consensus GYQW.
C5

FIG. 1 cont.

1 70

H15	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
B210	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
B2198	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGTCGTATCC	GAGCTCACAC
P20	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	AGTCGTATCC	GAGCTCACAC
H38	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
Z2491	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
H41	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
EG329	ATGAACGAAA	TATTGCGCAT	CATTGGAAT	AGCGCCCTCA	ATGCCTGGGT	CGTTGTATCC	GAGCTCACAC
PMC21	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCATGGGT	CGTCGTATCC	GAGCTCACAC
EG327	ATGAACAAAA	TATACCGCAT	CATTGGAAT	AGTGCCCTCA	ATGCCTGGGT	CGCCGTATCC	GAGCTCACAC
Consensus	ATGAAC-AAA	TAT--CGCAT	CATTGGAAT	AG-GCCCTCA	ATGC-TGGGT	-G--GTATCC	GAGCTCACAC

C1

71 140

H15	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
B210	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
B2198	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
P20	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
H38	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
Z2491	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
H41	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
EG329	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT
PMC21	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGAAGACCGC	CGTATTGGCG	ACTCTGTTGT	TTGCAACGGT
EG327	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TGGCGACCGC	CGTATTGGCG	ACACTGTTGT	TTGCAACGGT
Consensus	GCAACCACAC	CAAACGCGCC	TCCGCAACCG	TG--GACCGC	CGTATTGGCG	AC-CTG-TGT	--GCAACGGT

C1

141 210

H15	TCAGGCCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
B210	TCAGGCCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
B2198	TCAGGCCGAAT	GCTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
P20	TCAGGCCGAAT	GCTACCGATA	CCGAT.....	..GAAGATGAA	GAGTTAGAA	CCGTAGCACG	CTCTGCTCTG
H38	TCAGGCCGAAT	GCTACCGATG	AAGAT.....	..GAAGAAGAA	GAGTTAGAAC	CCGTAGTACG	CTCTGCTCTG
Z2491	TCAGGCCGAAT	GCTACCGATG	AAGAT.....	..GAAGAAGAA	GAGTTAGAAC	CCGTACAACG	CTCTGCTCTG
H41	TCAGGCCGAAT	GCTACCGATG	AAGAT.....	..GAAGAAGAA	GAGTTAGAAC	CCGTACAACG	CTCTG...TC
EG329	TCAGGCCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTGCTACG	CACTGTTGCC
PMC21	TCAGGCCAAGT	GCTAACAATG	AAGAGCAAGA	AGAAGATTTA	TATTTAGACC	CCGTACAACG	CACTGTTGCC
EG327	TCAGGCCGAGT	ACTACCGATG	ACGAC.....GATTTA	TATTTAGAAC	CCGTACAACG	CACTGCTGTC
Consensus	TCAGGC-A-T	-CTA-C-AT-	--GA-----	----GA---A	-A-TTAGA--	CCGT---ACG	C-CTG-----

C1

V1

211 280

H15	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
B210	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
B2198	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG
P20	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	TCGAATCTAC	AGGAGA...T	ATAGGTTGGA
H38	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	ACGAATCTAC	AGGAAA...T	ATAGGTTGGA
Z2491	GGG...AGCAT	TCAAG.CCAG	TATGGAAGGC	AGCGGCGAAT	TGGAAACGAT	ATCAT...T	ATCAATGACT
H41	GTAGGGAGCA	TTCAGCCAG	TATGGAAGGC	AGCGTCAAT	TGGAAACGAT	A.....	TCATTATCAA
EG329	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG
PMC21	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG
EG327	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGTTAC	AGAAGA...T	TCAAATTGGG
Consensus	G-----	T-----C--	TA--GAAGGC	A--G--GAA-	--GAA-----	A-----	-----

V1

FIG. 2

	281								350
H15	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
BZ10	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
BZ198	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
P20	GTATATATTA	CGACGATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA		
H38	GTATATATTA	CGACAAACAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA		
Z2491	AACGACAGCA	AGGAATTTGT	AGACCCATAC	ATAGTA....	.GTACCCTC	AAAGCCGGCG	ACAACCTGAA		
H41	TGACTAACGA	CAGCAAGGAA	TTGTAGACC	CATACATAGT	AGTTACCCTC	AAAGCCGGCG	ACAACCTGAA		
EG329	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
PMC21	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
EG327	GAGTATATTT	CGACAAAGAA	GGAGTACTAA	CAGCCGGAAC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
Consensus	-----A-----	-----A-----	-----A-----	-----A-----	-----T-ACCCTC-----	-----AAGCCGGCG-----	-----ACAACTGAA-----		
				V1		C2			
	351								420
H15	AATCAAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA		
BZ10	AATCAAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA		
BZ198	AATCAAAACAA	AACACCAATG	AAAACACC..	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA		
P20	AATCAAAACAA	AGCGGCAAG	A.....CTTCACCTA	CTCGCTGAAA		
H38	AATCAAAACAA	AACACCAATA	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCGCTGAAA		
Z2491	AATCAAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA		
H41	AATCAAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA		
EG329	AATCAAAACAA	AAC.....G..GCACAA	ACTTCACCTA	CTCGCTGAAA		
PMC21	AATCAAAACAA	AAC.....G..GCACAA	ACTTCACCTA	CTCGCTGAAA		
EG327	AATCAAAACAA	AACACCAATG	AAAACACC..	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA		
Consensus	AATCAAAACAA	A-C-----	-----A-----	-----A-----	-----AATGCCAGTA-----	-----CTTCACCTA-----	-----CTC-CTGAAA-----		
	C2		V2			C3			
	421								490
H15	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
BZ10	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
BZ198	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
P20	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
H38	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
Z2491	AAAGACCTCA	CAGGCTGAT	CAATGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
H41	AAAGACCTCA	CAGGCTGAT	CAATGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
EG329	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
PMC21	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
EG327	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAACGGT	AATAAAGTCA		
Consensus	AAAGACCTCA	-AG--CTGA-	CA-TGTTG-A	ACTGAAAAAT	TATCGTTT-G	CGCAAC-G-	AA-AAAGTCA		
				C3					
	491								560
H15	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
BZ10	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
BZ198	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
P20	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
H38	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
Z2491	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
H41	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
EG329	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
PMC21	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
EG327	ACATCACAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCACGGT		
Consensus	ACATCA-AAG	CGACACCAA	GGCTTGAATT	T-GCGAAA-A	AACGGCTG-G	AC-AACGGCG	AC-CCACGGT		
				C3					
	561								630
H15	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC		
BZ10	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC		
BZ198	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC		
P20	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTT	GCGGGTTCTT	CTGCTTCTCA	CGTTGATGCG		
H38	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC		
Z2491	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTT	GCGGGTTCTT	CTGCTTCTCA	CGTTGATGCG		
H41	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC		
EG329	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC		
PMC21	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC		
EG327	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC		
Consensus	TCATCTGAAC	GCTAT--GGT	CGACTTTGAC	CGATA-GCT-	--G--T-C--	--GC--C--	---G---C-		
		C3			V3				

FIG. 2 cont.

631 700

H15	AACGACAACG	TTACCGATGA	CGAGAAAAA	CGTGGCGCAA	CGGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ10	AACGACAACG	TTACCGATGA	CGAGAAAAA	CGTGGCGCAA	CGGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ198	AACGACAACG	TTACCGATGA	CGAGAAAAA	CGTGGCGCAA	CGGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
P20	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGGCGCAA	GTATTAAAGA	TGTGTTGAAT	CGCGGTTGGA
H38	AACGACAACG	TTACCGATGA	CGAGAAAAA	CGTGGCGCAA	CGGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Z2491	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGGCGCAA	GTATTAAAGA	TGTGTTGAAT	CGCGGTTGGA
H41	AACGACAACG	TTACCGATGA	CGAGAAAAA	CGTGGCGCAA	CGGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
EG329	AACGACAACG	TTACCGATGA	CGAGAAAAA	CGTGGCGCAA	CGGTTAAAGA	CGTATTAAAC	GCTGGCTGGA
PMC21	AACGACAACG	TTACCGATGA	CGAGAAAAA	CGTGGCGCAA	CGGTTAAAGA	CGTATTAAAC	GCTGGCTGGA
EG327	AACGACAACG	TTACCGATGA	CGAGAAAAA	CGTGGCGCAA	CGGTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Consensus	---AC-A---	-TAC--AT-A	C-----A--	CGTGC-GCAA	G--TTAA-GA	-GT-TT-AA-	GC-GG-TGGA

V3 C4

701 770

H15	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCTGTC	GCACCTACGA
BZ10	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTC	GATTTCTGTC	GCACCTACGA
BZ198	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCTGTC	GCACCTACGA
P20	ATATTAAAGG	TGTTAAACT	GGTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCTGTC	GCACCTACGA
H38	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCTGTC	GCACCTACGA
Z2491	ATATTAAAGG	TGTTAAACT	GGTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCTGTC	GCACCTACGA
H41	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCTGTC	GCACCTACGA
EG329	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCTGTC	GCACCTACGA
PMC21	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCTGTC	GCACCTACGA
EG327	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCTGTC	GCACCTACGA
Consensus	A-ATTAA-GG	-GTTAA-C-	GG--CAACA-	CT-----TC	-GA-AA-GT-	GATTTCTGTC	-GACTTACGA

C4 V4 C5

771 840

H15	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ10	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ198	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
P20	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H38	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Z2491	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H41	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG329	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
PMC21	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG327	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Consensus	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG

C5

841 910

H15	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ10	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ198	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
P20	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H38	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Z2491	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H41	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG329	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
PMC21	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG327	AAAACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Consensus	A-AACCGAAG	TTAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA

C5

911 980

H15	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
BZ10	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
BZ198	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
P20	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
H38	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
Z2491	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
H41	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
EG329	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
PMC21	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
EG327	AAGGCAAAAG	CGAGAATGGT	TCTTCTACAG	ACGAAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA
Consensus	AAG-CABAG-	CGAGAATG-T	TCTTCTACAG	AC-AAGGCCA	AGGCTTAGTG	ACTGCAAAAG	AAGTGATTGA

C5

FIG. 2 cont.

981 1050

H15	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
B210	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
BZ198	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
P20	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H38	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Z2491	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
H41	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG329	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
PMC21	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
EG327	TGCAGTAAAC	AAGGCTGGTT	GGAGAATGAA	AACAACAACC	GCTAATGGTC	AAACAGGTCA	AGCTGACAAG
Consensus	<u>TGCAGTAAAC</u>	<u>AAGGCTGGTT</u>	<u>GGAGAATGAA</u>	<u>AACAACAACC</u>	<u>GCTAATGGTC</u>	<u>AAACAGGTCA</u>	<u>AGCTGACAAG</u>

C5

1051 1120

H15	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
B210	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
BZ198	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
P20	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
H38	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
Z2491	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
H41	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
EG329	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
PMC21	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
EG327	TTTGAAACCG	TTACATCAGG	CACAAAAGTA	ACCTTTGCTA	GTGGTAATGG	TACAACCTGG	ACTGTAAGTA
Consensus	<u>TTTGAAACCG</u>	<u>TTACATCAGG</u>	<u>CACAAAAGTA</u>	<u>ACCTTTGCTA</u>	<u>GTGGTAATGG</u>	<u>TACAACCTGG</u>	<u>ACTGTAAGTA</u>

C5

1121 1190

H15	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
B210	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
BZ198	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
P20	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H38	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Z2491	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
H41	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG329	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
PMC21	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
EG327	AAGATGATCA	AGGCAACATC	ACTGTTAAGT	ATGATGTAAA	TGTCGGCGAT	GCCCTAAACG	TCAATCAGCT
Consensus	<u>AAGATGATCA</u>	<u>AGGCAACATC</u>	<u>ACTGTTAAGT</u>	<u>ATGATGTAAA</u>	<u>TGTCGGCGAT</u>	<u>GCCCTAAACG</u>	<u>TCAATCAGCT</u>

C5

1191 1260

H15	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
B210	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
BZ198	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
P20	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H38	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Z2491	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
H41	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG329	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
PMC21	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
EG327	GCAAAACAGC	GGTTGGAATT	TGGATTCCAA	AGCGGTTGCA	GGTTCTTCGG	GCAAAGTCAT	CAGCGGCAAT
Consensus	<u>GCAAAACAGC</u>	<u>GGTTGGAATT</u>	<u>TGGATTCCAA</u>	<u>AGCGGTTGCA</u>	<u>GGTTCTTCGG</u>	<u>GCAAAGTCAT</u>	<u>CAGCGGCAAT</u>

C5

1261 1330

H15	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
B210	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
BZ198	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
P20	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H38	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Z2491	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
H41	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG329	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
PMC21	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
EG327	GTTTCGCCGA	GCAAGGGAAA	GATGGATGAA	ACCGTCAACA	TTAATGCCGG	CAACAACATC	GAGATTACCC
Consensus	<u>GTTTCGCCGA</u>	<u>GCAAGGGAAA</u>	<u>GATGGATGAA</u>	<u>ACCGTCAACA</u>	<u>TTAATGCCGG</u>	<u>CAACAACATC</u>	<u>GAGATTACCC</u>

C5

FIG. 2 cont.

1331 1400

H15	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
B210	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
B2198	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
P20	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
H38	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
Z2491	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
H41	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
EG329	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
PMC21	GCAACGGTAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
EG327	GCAACGGCAA	AAATATCGAC	ATCGCCACTT	CGATGACCCC	GCAATTTTCC	AGCGTTTCGC	TCGCGCGGG
Consensus	<u>GCAACGG-AA</u>	<u>AAATATCGAC</u>	<u>ATCGCCACTT</u>	<u>CGATG-C-CC</u>	<u>GCA-TTTTC</u>	<u>AGCGTTTCGC</u>	<u>TCGG-GCGGG</u>

C5

1401 1470

H15	GCGGATGCG	CCCACITTA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
B210	GCGGATGCG	CCCACITTA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
B2198	GCGGATGCG	CCCACITTA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
P20	GCGGATGCG	CCCACITTA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
H38	GCGGATGCG	CCCACITTA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
Z2491	GCGGATGCG	CCCACITTA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
H41	GCGGATGCG	CCCACITTA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
EG329	GCGGATGCG	CCCACITTA	GCGTGGAT..	.GGGACGCA	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
PMC21	GCGGATGCG	CCCACITTA	GCGTGGAT..	.GGGACGCA	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
EG327	GCGGATGCG	CCCACITTA	GCGTGGATGA	CGAGGGCGCG	TTGAATGTTCG	GCAGCAAGGA	TGCCAACAAA
Consensus	<u>GCG-GATGCG</u>	<u>CCCACITTA</u>	<u>GCGTGGAT--</u>	<u>---GGC-</u>	<u>TTGAATGTTCG</u>	<u>GCAGCAAG-A</u>	<u>---CAACAAA</u>

C5

1471 1540

H15	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
B210	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
B2198	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
P20	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
H38	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
Z2491	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
H41	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
EG329	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
PMC21	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
EG327	CCCGTCCGCA	TTACCAATGT	CGCCCCGGGC	GTTAAAGAGG	GGGATGTTAC	AAACGTCCGA	CAACTTAAAG
Consensus	<u>CCCGTCCGCA</u>	<u>TTACCAATGT</u>	<u>CGCCCCGGGC</u>	<u>GTTAAAGAGG</u>	<u>GGGATGTTAC</u>	<u>AAACGTCCG-</u>	<u>CAACTTAAAG</u>

C5

1541 1610

H15	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCAAGC
B210	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCAAGC
B2198	CGGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC
P20	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGCGCGGGTA	TCGCCCAAGC
H38	CGGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC
Z2491	CGGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC
H41	GTGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC
EG329	CGGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC
PMC21	CGGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC
EG327	CGGTGGCGCA	AAACTTGAAC	AACCGCATCG	ACAATGTGGA	CGGCAACGCG	CGTGC GGGA	TCGCCCAAGC
Consensus	<u>G-GTGGCGCA</u>	<u>AAACTTGAAC</u>	<u>AACCGCATCG</u>	<u>ACAATGTG-A</u>	<u>CGGCAACGCG</u>	<u>CG-GCGGG-A</u>	<u>TCGCCCAAGC</u>

C5

1611 1680

H15	GATTGCAACC	GCAGGTCTGG	CTCAGGCCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
B210	GATTGCAACC	GCAGGTCTGG	CTCAGGCCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
B2198	GATTGCAACC	GCAGGTCTAG	TTTCCAGGCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
P20	GATTGCAACC	GCAGGTCTGG	CTCAGGCCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
H38	GATTGCAACC	GCAGGTCTGG	TTTCCAGGCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
Z2491	GATTGCAACC	GCAGGTCTGG	TTTCCAGGCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
H41	GATTGCAACC	GCAGGTCTGG	TTTCCAGGCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
EG329	GATTGCAACC	GCAGGTCTGG	TTTCCAGGCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
PMC21	GATTGCAACC	GCAGGTCTGG	TTTCCAGGCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
EG327	GATTGCAACC	GCAGGTCTGG	TTTCCAGGCTA	TTTGCCCGGC	AAGAGTATGA	TGGCGATCGG	CGGCGGTACT
Consensus	<u>GATTGCAACC</u>	<u>GCAGGT-T-G</u>	<u>-TCAGGC-TA</u>	<u>T-TGCCCGGC</u>	<u>AAGAGTATGA</u>	<u>TGGCGATCGG</u>	<u>CGGCG--ACT</u>

C5

FIG. 2 cont.

	1681						1750
H15	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCGAGCA	TTTCTGACAC	TGGGAATTGG	GTTATCAAGG
BZ10	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCGAGCA	TTTCTGACAC	TGGGAATTGG	GTTATCAAGG
BZ198	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCAAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG
P20	TATCTCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCGAGCA	TTTCTGACAC	TGGGAATTGG	GTTATCAAGG
H38	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG
Z2491	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG
H41	TATCTCGGCG	AAGCCGGTTA	TGCCATCGGC	TACTCAAGCA	TTTCCGCGGG	CGGAAATTGG	ATTATCAAAG
EG329	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG
PMC21	TATCGCGGCG	AAGCCGGTTA	CGCCATCGGC	TACTCCAGTA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG
EG327	TATCGCGGCG	AAGCCGGTTA	TGCCATCGGC	TACTCAAGCA	TTTCCGACGG	CGGAAATTGG	ATTATCAAAG
Consensus	<u>TATC-CGGCG</u>	<u>AAGCCGGTTA</u>	<u>-GCCATCGGC</u>	<u>TACTC-AG-A</u>	<u>TTTC-G-C--</u>	<u>-GG-AATTGG</u>	<u>-TTATCAA-G</u>

C5

	1751						1815
H15	GCACGGCTTC	CGGCAATTCC	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
BZ10	GCACGGCTTC	CGGCAATTCC	CGCGGTCATT	TCGGTACTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
BZ198	GCACGGCTTC	CGGCAATTCC	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAAT	GGTAA
P20	GCACGGCTTC	CGGCAATTCC	CGCGGTCATT	TCGGTACTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
H38	GCACGGCTTC	CGGCAATTCC	CGCGGTCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
Z2491	GCACGGCTTC	CGGCAATTCC	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
H41	GCACGGCTTC	CGGCAATTCC	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
EG329	GCACGGCTTC	CGGCAATTCC	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
PMC21	GCACGGCTTC	CGGCAATTCC	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
EG327	GCACGGCTTC	CGGCAATTCC	CGCGGCCATT	TCGGTGCTTC	CGCATCTGTC	GGTTATCAGT	GGTAA
Consensus	<u>GCACGGCTTC</u>	<u>CGGCAATTCC</u>	<u>CGCGG-CATT</u>	<u>TCGGT-CTTC</u>	<u>CGCATCTGTC</u>	<u>GGTTATCA-T</u>	<u>GGTAA</u>

C5

FIG. 2 cont.

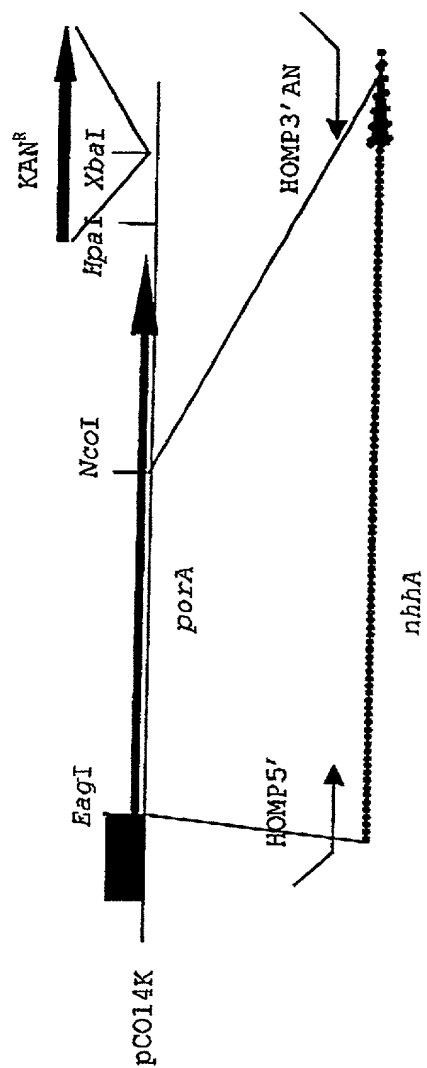


FIG. 3A

PIP52 (PMC21)

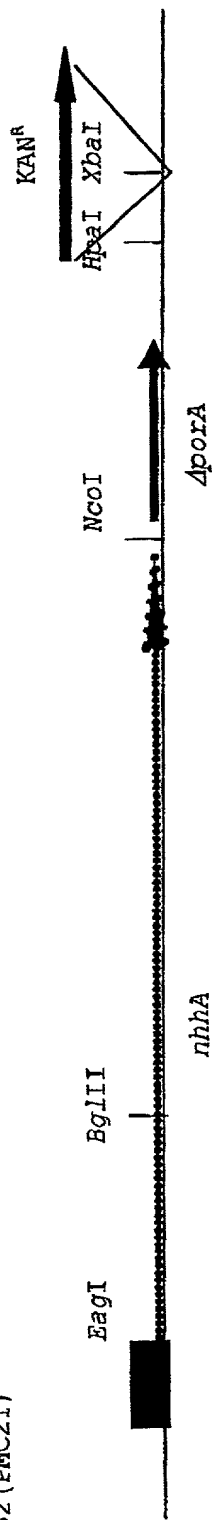


FIG. 3B

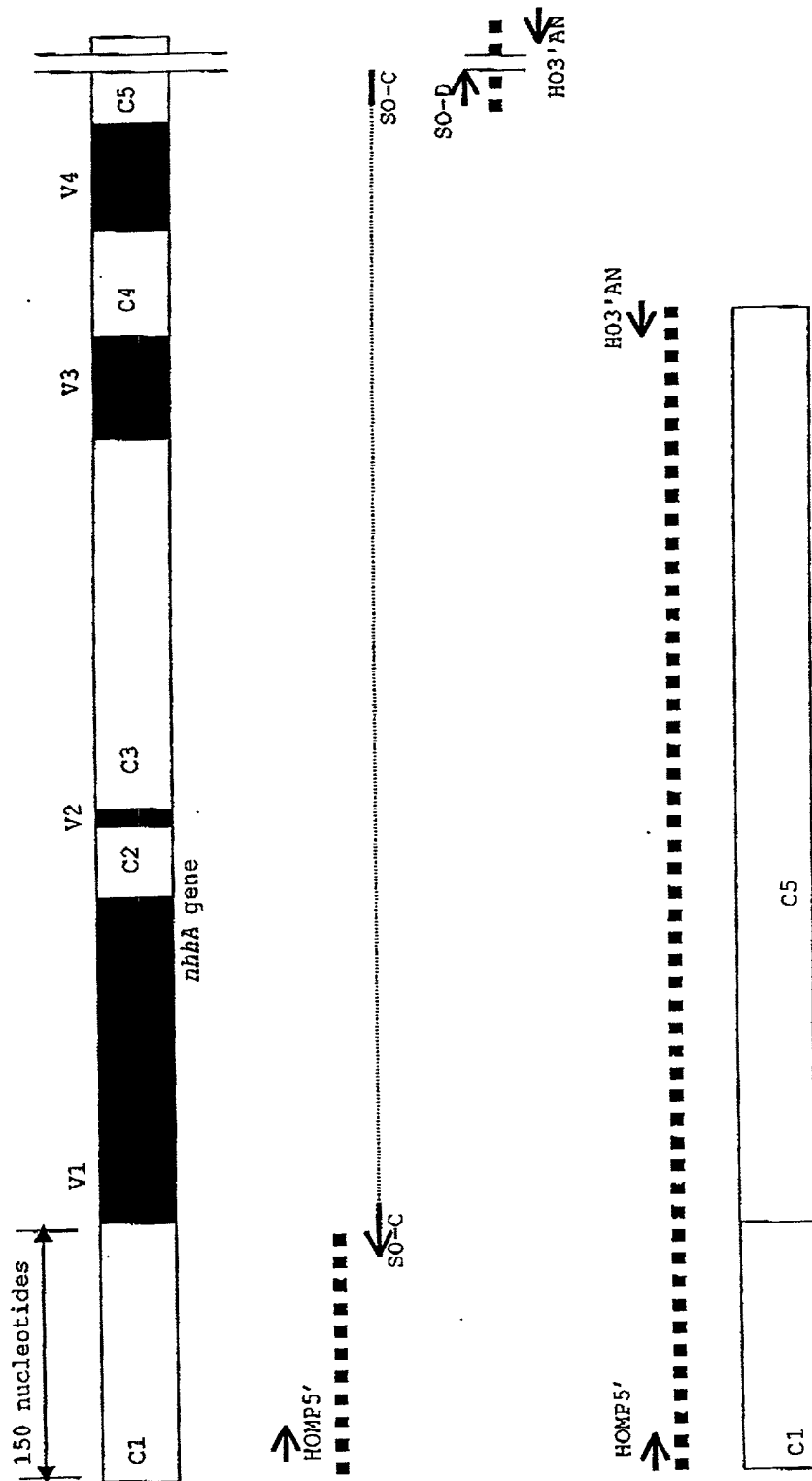


FIG. 4A

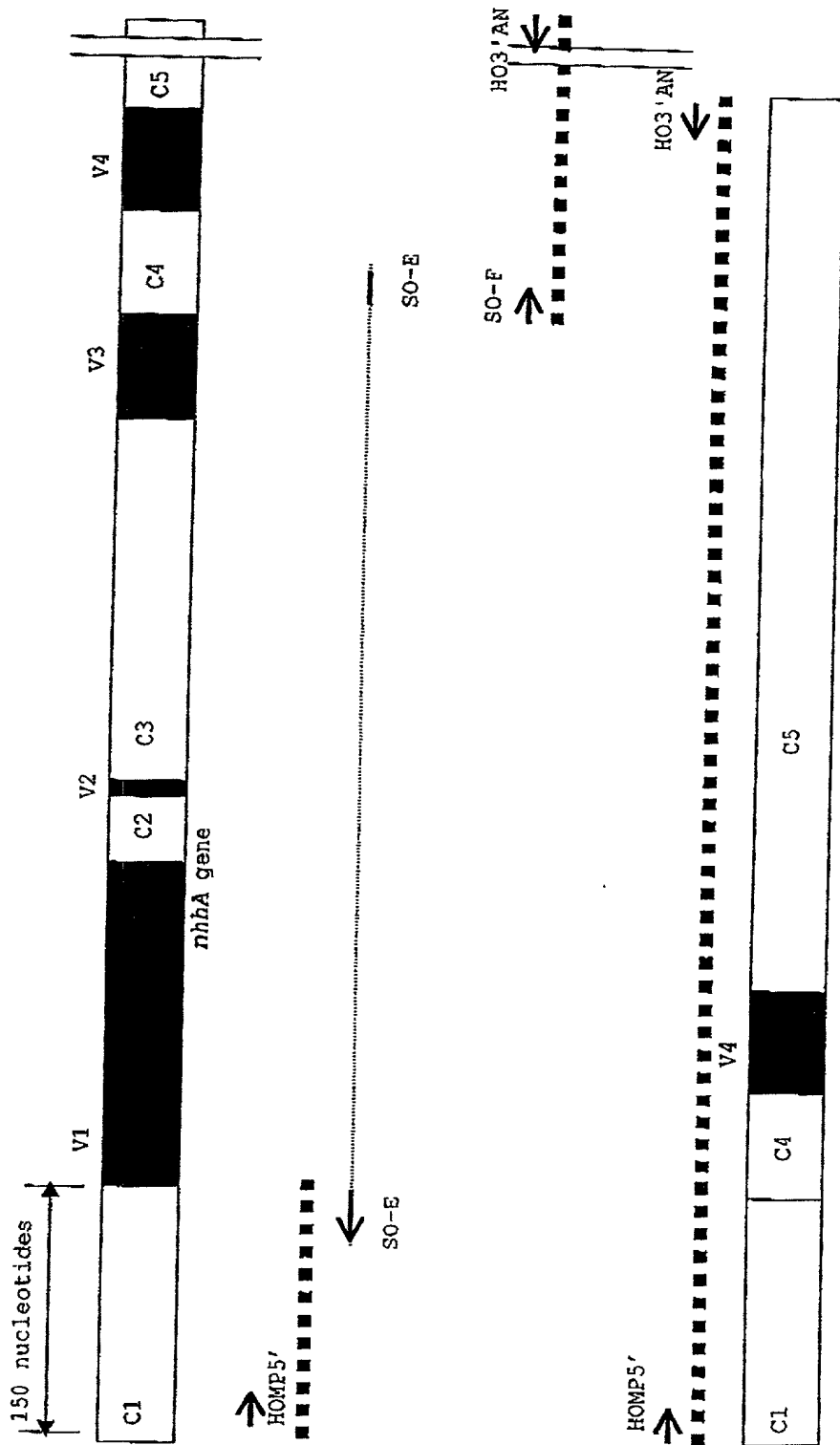
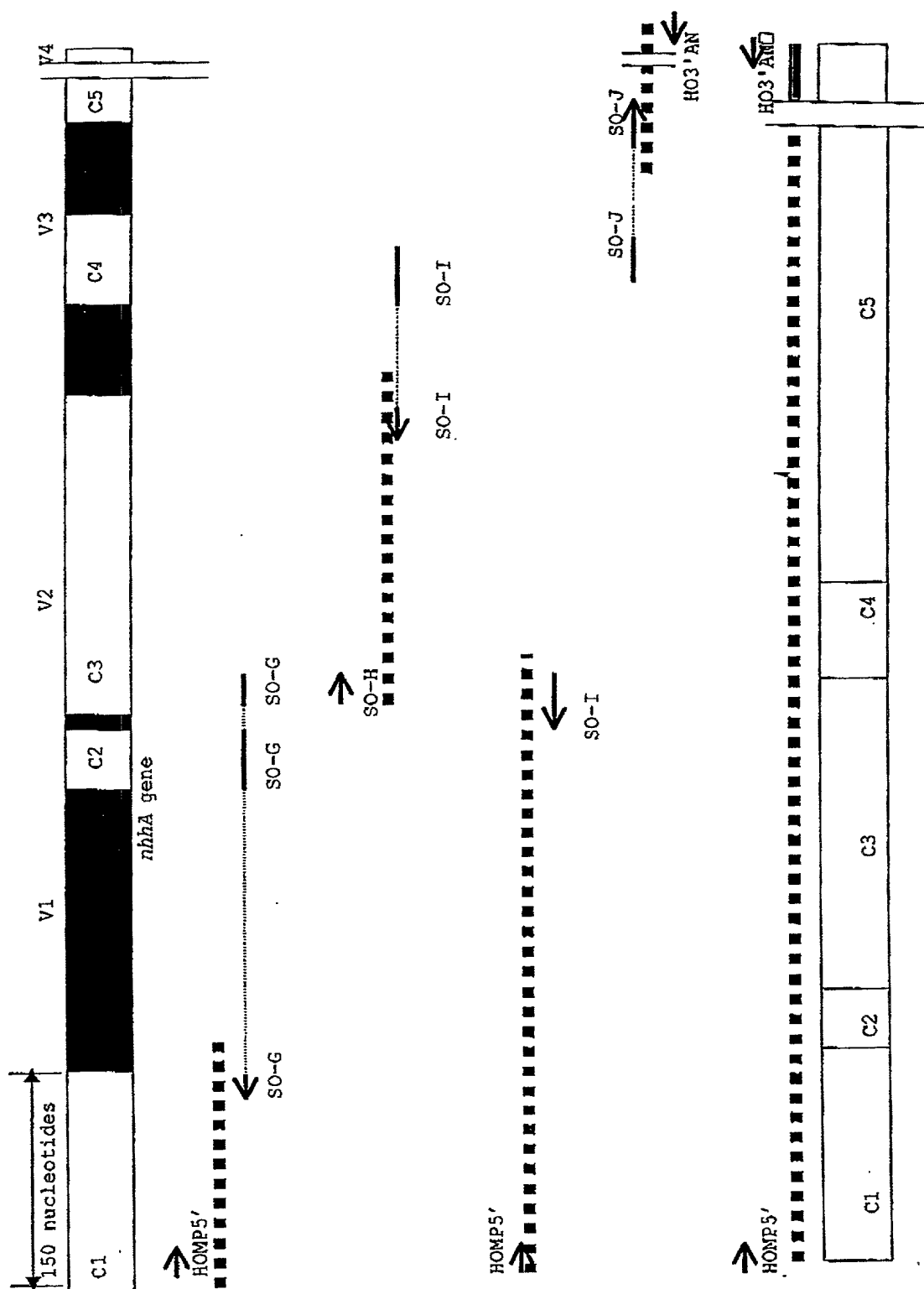


FIG. 4B



1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGD TTVHL
 101 NGIGSTLTD T LLNTGATTNV TNDNVTDDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEKDGLKV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKT TTA
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WNLDSKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKDKNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQNINNR IDNV DGNARA GIAQAIATAG
 451 LVQAYLPKGS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
 501 HFGASASVGY QW*

A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACAAATG AAACAGATCT GACCAAGTGT GGAAC TGA AAATTATCGTT
 201 TAGCGCAAAC GGCAATAAAG TCAACATCAC AAGCGACACC AAAGGCTTGA
 251 ATTTTGCGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
 301 AACGGTATTG GTTCGACTTT GACCGATACG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
 401 CAAGCGTTAA AGACGTATTA AACGCTGGCT GGAACATTA AGGCGTTAAA
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
 551 GCAAAGACAA CGGCAAGAAA ACCGAAGTTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG ACAAGGCGA
 651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGA CT GCAAAGAAG
 701 TGATTGATGC AGTAAACAAG GCTGGTTGGA GAATGAAAAC AACACCGCT
 751 AATGGTCAAA CAGETCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAATGTAACC TTTGCTAGTG GTAAAGGTAC AACTGCGACT GTAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTATGTATG ATGTAAATGT CGGCGATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTTGG ATTCCAAAGC
 951 GGTTGCAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
 1051 ATTACCCGCA ACGGTAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
 1101 GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTGAGCG
 1151 TGGATGGGGA CGCATTGAAT GTCGGCAGCA AGAAGGACAA CAAACCCGTC
 1201 CGCATTACCA ATGTCGCCCC GGGCGTTAAA GAGGGGGATG TTACAAACGT
 1251 CGCACAACTT AAAGGCGTGG CGCAAACTT GAACAACCGC ATCGACAATG
 1301 TGGACGGCAA CGCGCGTGCG GGCATCGCCC AAGCGATTGC AACC GCAGGT
 1351 CTGGTT CAGG CGTATTTGCC CGGCAAGAGT ATGATGGCGA TCGGCGGCGG
 1401 CACTTATCGC GCGGAAGCCG GTTACGCCAT CGGCTACTCC AGTATTTCCG
 1451 ACGGCGGAAA TTGGATTATC AAAGGCACGG CTTCCGGCAA TTCGCGCGGC
 1501 CATTTCCGGT CTTCCGCATC TGTCGGTTAT CAGTGGTAA

B

FIG. 5

1 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAFLA TLLFATVQAN
 51 ATDETLGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGDITTVHL
 101 NGIGSTLTDM LLNTGATTNV TNDNVTDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKKEDGKLV TGKRGGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTITTA
 251 NGQTGQADKF ETVTSGTKVT FASNGGTTAT VSKDDQGNIT VKYDVNVGDA
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGMDET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
 451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
 501 GHFGASASVG YQW*

A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCCTGGGT
 51 CGCCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACACTGTTGT TTGCAACGGT TCAGGCGAAT
 151 GCTACCGATG AAACAGGCCT GATCAATGTT GAAACTGAAA AATTATCGTT
 201 TGGCGCAAAAC GGCAAGAAAG TCAACATCAT AAGCGACACC AAAGGCTTGA
 251 ATTTGCGGAA AGAAACGGCT GGGACGAACG GCGACACCAC GGTTCATCTG
 301 AACGGTATCG GTTCGACTTT GACCGATATG CTGCTGAATA CCGGAGCGAC
 351 CACAAACGTA ACCAACGACA ACGTTACCGA TGACGAGAAA AAACGTGCGG
 401 CAAGCGTTAA AGACGTATTA AACGCAGGCT GGAACATTAA AGGCGTTAAA
 451 CCCGGTACAA CAGCTTCCGA TAACGTTGAT TTCGTCCGCA CTTACGACAC
 501 AGTCGAGTTC TTGAGCGCAG ATACGAAAAC AACGACTGTT AATGTGGAAA
 551 GCAAAGACAA CGGCAAGAAA ACCGAAAGTA AAATCGGTGC GAAGACTTCT
 601 GTTATTAAAG AAAAAGACGG TAAGTTGGTT ACTGGTAAAG GCAAAGGCGA
 651 GAATGGTTCT TCTACAGACG AAGGCGAAGG CTTAGTGACT GCAAAGAAG
 701 TGATTGATGC AGTAAACAAG GCTGTTGGA GAATGAAAAC AACAACCGCT
 751 AATGGTCAA CAGGTCAAGC TGACAAGTTT GAAACCGTTA CATCAGGCAC
 801 AAAAGTAACC TTTGCTAGTG GTAATGGTAC AACTGCGACT GTAAGTAAAG
 851 ATGATCAAGG CAACATCACT GTTAAGTATG ATGTAAATGT CGGCGATGCC
 901 CTAAACGTCA ATCAGCTGCA AAACAGCGGT TGGAAATTTGG ATTCCAAAGC
 951 GGTTCGAGGT TCTTCGGGCA AAGTCATCAG CGGCAATGTT TCGCCGAGCA
 1001 AGGGAAAGAT GGATGAAACC GTCAACATTA ATGCCGGCAA CAACATCGAG
 1051 ATTACCCGCA ACGGCAAAAA TATCGACATC GCCACTTCGA TGACCCCGCA
 1101 ATTTTCCAGC GTTTCGCTCG GCGCGGGGGC GGATGCGCCC ACTTTAAGCG
 1151 TGGATGACGA GGGCGCGTTG AATGTCGGCA GCAAGGATGC CAACAAACCC
 1201 GTCCGCATTA CCAATGTCGC CCCGCGCGTT AAAGAGGGGG ATGTTACAAA
 1251 CGTCGCGCAA CTAAAGGTG TGGCGCAAAA CTTGAACAAC CGCATCGACA
 1301 ATGTGAACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT TGCAACCGCA
 1351 GGTCTGGTTC AGGCGTATCT GCGCGGCAAG AGTATGATGG CGATCGGCGG
 1401 CGGCACTTAT CTCGGCGAAG CCGGTTATGC CATCGGCTAC TCAAGCATTT
 1451 CCGCCGCGCG AAATTGGATT ATCAAAGGCA CGGCTTCCGG CAATTGCGCG
 1501 GGCCATTTTC GTGCTTCCGC ATCTGTCGGT TATCAGTGGT AA

B

FIG. 6

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAIVLA TLLFATVQAS
 51 ANNVDFVRTY DTVEELSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
 101 DGKLVGTGDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
 151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
 201 LQNSGWNLDL KAVAGSSGKV ISGNVSPSKG KMDETVNINA GNNIEITRNG
 251 KNIDIATSMT PQFSSVSLGA GADAPTLSDV GDALNVGSKK DNKPVRTITV
 301 APGVKEGDVT NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
 351 LPGKSMMAIG GGTyrGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
 401 ASVGyQW*

A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACAACG TTGATTTTCGT CCGCACTTAC GACACAGTCG AGTTCCTTGAG
 201 CGCAGATACG AAAACAACGA CTGTTAATGT GGAAAGCAAA GACAACGGCA
 251 AGAAAACCGA AGTTAAAATC GGTGCGAAGA CTTCTGTTAT TAAAGAAAAA
 301 GACGGTAAGT TGGTTACTGG TAAAGACAAA GGCAGAAATG GTTCTTCTAC
 351 AGACGAAGGC GAAGGCTTAG TGACTGCAAA AGAAGTGATT GATGCAGTAA
 401 ACAAGGCTGG TTGGAGAATG AAAACAACAA CCGCTAATGG TCAACAGGT
 451 CAAGCTGACA AGTTTGAAAC CGTTACATCA GGCACAAATG TAACCTTTGC
 501 TAGTGGTAAA GGTACAACG CCACTGTAAG TAAAGATGAT CAAGGCAACA
 551 TCACTGTTAT GTATGATGTA AATGTCGGCG ATGCCCTAA CGTCAATCAG
 601 CTGCAAAACA CCGGTTGGAA TTTGGATTCC AAAGCGGTTG CAGGTTCTTC
 651 GGGCAAAGTC ATCAGCGGCA ATGTTTCGCC GAGCAAGGGA AAGATGGATG
 701 AAACCGTCAA CATTAATGCC GGCAACAACA TCGAGATTAC CCGCAACGGT
 751 AAAAATATCG ACATCGCCAC TTCGATGACC CCGCAGTTT CCAGCGTTTC
 801 GCTCGGCGCG GGGGCGGATG CCGCCACTTT GAGCGTGGAT GGGGACGCAT
 851 TGAATGTCGG CAGCAAGAAG GACAACAAAC CCGTCCGCAT TACCAATGTC
 901 GCCCCGGGCG TTAAAGAGGG GGATGTTACA AACGTCGCAC AACTTAAAGG
 951 CGTGGCGCAA AACTTGAACA ACCGCATCGA CAATGTGGAC GGCAACGCGC
 1001 GTGCGGGCAT CCGCCAAGCG ATTGCAACCG CAGGTCTGGT TCAGGCGTAT
 1051 TTGCCCCGCA AGAGTATGAT GCGGATCGGC GCGGCGACTT ATCGCGGCGA
 1101 AGCCGGTTAC GCCATCGGCT ACTCCAGTAT TTCCGACGGC GGAAATTCGA
 1151 TTATCAAAGG CACGGCTTCC GGCAATTGCG GCGGCCATTT CCGTGCTTCC
 1201 GCATCTGTCT GTTATCAGTG GTAA

B

FIG. 7

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANRAASVKDV LNAGWNIKGV KPGTTASDNV DFRVRYDTVE FLSADTKTTT
 101 VNVESKDNGK KTEVKIGAKT SVIKEKDGKL VTGKDKGENG SSTDEGEGLV
 151 TAKEVIDAVN KAGWRMKTTT ANGQTGQADK FETVTSGTNV TFASGKGTTA
 201 TVSKDDQGNi TVMYDVNVGD ALNVNQLONS GWNLDKAVA GSSGKVISGN
 251 VSPSKGKMD E TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA
 301 PTLSDVDGAL NVGSKKDNKP VRITNVAPGV KEGDVINVAQ LKGVAQNLNN
 351 RIDNVDGNAR AGIAQAIATA GLVQAYLP GK SMMAIGGGTY RGEAGYAIGY
 401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW*

A

1 ATGAACAAAA TATACCGCAT CATTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCCAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACCGTG CGGCAAGCGT TAAAGACGTA TTAAACGCTG GCTGGAACAT
 201 TAAAGGCGTT AAACCCGGTA CAACAGCTTC CGATAACGTT GATTTCGTCC
 251 GCACTTACGA CACAGTCGAG TTCTTGAGCG CAGATACGAA AACACGACT
 301 GTTAATGTGG AAAGCAAAGA CAACGGCAAG AAAACCGAAG TTAAAATCGG
 351 TGCGAAGACT TCTGTTATTA AAGAAAAAGA CGGTAAGTTG GTTACTGGTA
 401 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACCAAGGCGA AGGCTTAGTG
 451 ACTGCAAAAG AAGTGATTGA TGCAGTAAAC AAGGCTGGTT GGAGAATGAA
 501 AACAAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG TTTGAAACCG
 551 TTACATCAGG CACAAATGTA ACCTTTGCTA GTGGTAAAGG TACAACTGCG
 601 ACTGTAAGTA AAGATGATCA AGGCAACATC ACTGTTATGT ATGATGTAAA
 651 TGTCGGCGAT GCCCTAAACG TCAATCAGCT GCAAAACAGC GGTGGAATT
 701 TGGATTCCAA AGCGGTTGCA GGTTCCTCGG GCAAAGTCAT CAGCGGCAAT
 751 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCCG
 801 CAACAACATC GAGATTACCC GCAACGGTAA AAATATCGAC ATCGCCACTT
 851 CGATGACCCC GCAGTTTTCC AGCGTTTCGC TCGGCGCGGG GCGGATGCG
 901 CCCACTTTGA GCGTGGATGG GGACGCATTG AATGTCGGCA GCAAGAAGGA
 951 CAACAAACCC GTCCGCATTA CCAATGTCGC CCCGGGCGTT AAAGAGGGGG
 1001 ATGTTACAAA CGTCGCACAA CTAAAGGCG TGGCGCAAAA CTTGAACAAC
 1051 CGCATCGACA ATGTGGACGG CAACGCGCGT GCGGGCATCG CCCAAGCGAT
 1101 TGCAACCGCA GGTCTGGTTC AGGCGTATTT GCGCGCAAG AGTATGATGG
 1151 CGATCGGCGG CGGCACTTAT CGCGGCGAAG CCGGTTACGC CATCGGCTAC
 1201 TCCAGTATTT CCGACGGCGG AAATTGGATT ATCAAAGGCA CGGCTTCCGG
 1251 CAATTCGCGC GGCCATTTCC GTGCTTCCGC ATCTGTCGGT TATCAGTGGT
 1301 AA

B

FIG. 8

1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVQAS
 51 ANTLKAGDNL KIKQFTYSLK KDLTDITSVG TEKLSFSANG NKVNITSDTK
 101 GLNFAKETAG TNGDTTVHLN GIGSTLTDRASVVKDVLNAG WNIKGVKNVD
 151 FVRTYDTVEF LSADTKTTTV NVEKDNKGK TEVKIGAKTS VIKEDGKLV
 201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA NGQTGQADKE
 251 ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA LNVNQLQNSG
 301 WNLDKAVAG SSGKVISGNV SPSKGMDET VNINAGNNIE ITRNGKNIDI
 351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
 401 EGDVTNVAQL KGVAQNLNLR IDNVGNARA GIAQAIATAG LVQAYLEPGKS
 451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY
 501 QW*

A

1 ATGAACAAAA TATACCGCAT CATTTGGAAT AGTGCCCTCA ATGCATGGGT
 51 CGTCGTATCC GAGCTCACAC GCAACCACAC CAAACGCGCC TCCGCAACCG
 101 TGAAGACCGC CGTATTGGCG ACTCTGTTGT TTGCAACGGT TCAGGCAAGT
 151 GCTAACACCC TCAAAGCCGG CGACAACCTG AAAATCAAAC AATTACCTA
 201 CTCGCTGAAA AAAGACCTCA CAGATCTGAC CAGTGTGGA ACTGAAAAAT
 251 TATCGTTTAG CGCAACGCGC AATAAAGTCA ACATCACAAG CGACACCAA
 301 GGCTTGAATT TTGCGAAAGA AACGGCTGGG ACGAACGCGC ACACCACGGT
 351 TCATCTGAAC GGTATTGGTT CGACTTTGAC CGATCGTGCG GCAAGCGTTA
 401 AAGACGTATT AAACGCTGGC TGGAACATTA AAGGCGTTAA AAACGTTGAT
 451 TTCGTCCGCA CTTACGACAC AGTCGAGTTC TTGAGCGCAG ATACGAAAAC
 501 AACGACTGTT AATGTGGAAA GCAAAGACAA CGGCAAGAAA ACCGAAGTTA
 551 AAATCGGTGC GAAGACTTCT GTTATTAAAG AAAAAGACGG TAAGTTGGTT
 601 ACTGGTAAAG ACAAAGGCCA GAATGGTTCT TCTACAGACG AAGGCGAAGG
 651 CTTAGTGAAC GCAAAGAAG TGATTGATGC AGTAAACAAG GCTGGTTGGA
 701 GAATGAAAAC AACAACCGCT AATGGTCAAA CAGGTCAAGC TGACPAAGTTT
 751 GAAACCGTTA CATCAGGCAC AAATGTAACC TTTGCTAGTG GTAAAGGTAC
 801 AACTGCGACT GTAAGTAAAG ATGATCAAGG CAACATCACT GTTATGTATG
 851 ATGTAAATGT CGGCGATGCC CTAAACGTCA ATCAGCTGCA AAACAGCGGT
 901 TGGAATTTGG ATTCCAAAAG GGTTCAGGT TCTTCGGGCA AAGTCATCAG
 951 CGGCAATGTT TCGCCGAGCA AGGGAAAGAT GGATGAAACC GTCAACATTA
 1001 ATGCCGGCAA CAACATCGAG ATTACCCGCA ACGGTAAAAA TATCGACATC
 1051 GCCACTTCGA TGACCCCGCA GTTTTCCAGC GTTTCGCTCG GCGCGGGGGC
 1101 GGATGCGCCC ACTTTGAGCG TGGATGGGGA CGCATTGAAT GTCGGCAGCA
 1151 AGAAGGACAA CAAACCCGTC CGCATTACCA ATGTCGCCCC GGGCGTTAA
 1201 GAGGGGGATG TTACAAACGT CGCACAACTT AAAGGCGTGG CGCAAACTT
 1251 GAACAACCGC ATCGACAATG TGGACGGCAA CGCGCGTGCG GGCATCGCCC
 1301 AAGCGATTGC AACCGCAGGT CTGGTTCAGG CGTATTTGCC CGGCAAGAGT
 1351 ATGATGGCGA TCGGCGGCGG CACTTATCGC GCGGAAGCCG GTTACGCCAT
 1401 CGGCTACTCC AGTATTTCCG ACGGCGGAAA TTGGATTATC AAAGGCACGG
 1451 CTTCCGGCAA TTCGCGCGGC CATTTCCGGT CTTCCGCATC TGTCGGTTAT
 1501 CAGTGGTAA

B

FIG. 9

1 50

H41 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN

PMC21 MNKIYRIIWN SALNAWVVVS DLTRNHTKRA SATUNTAVLA TLLFATVOAS

H41Studel MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN

PMC21Bglde1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS

PMC21C1C5 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS

C1

51 100

H41 ATDED...EE ELESVQRS.V VGSIOASMEG SVELET...I SLSMTNDSKE

PMC21 ANNEEQEYYL YLHPVQRTVA VLIIVNSDKEG AGEKEKVEEN SDWAVYFNEK

H41Studel ATDE.....

PMC21Bglde1 ANNE.....

PMC21C1C5 AN.....

V1

101 150

H41 FVDPYIVVTL KAGDNLKIKO N.TNENTNAS SFTYSLKKDL TGLINVETEK

PMC21 GVLTAETITL KAGDNLKIKO NGTN.....FTYSLKKDL TDLTSVGTEK

H41StudelTGLINVETEK

PMC21Bglde1TDLTSVGTEK

PMC21C1C5

V1 C2 V2 C3

151 200

H41 LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT

PMC21 LSFSAHGKVK NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT

H41Studel LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT

PMC21Bglde1 LSFSAHGKVK NITSDTKGLN FAKETAGTNG DTTVHLNGIG STLTDTLLNT

PMC21C1C5

C3 V3

201 250

H41 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

PMC21 GATTNVTNDN VTODEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

H41Studel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

PMC21Bglde1 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT

PMC21C1C5NVDFVRT

V3 C4 V4 C5

251 300

H41 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTKGK

PMC21 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTKGD

H41Studel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTKGK

PMC21Bglde1 YDTVEFLSAD TKTTTVNVES KONGKKTEVK IGAKTSVIKE KDGKLVTKGD

PMC21C1C5 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVTKGD

C5

301 350

H41 KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

PMC21 KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

H41Studel KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

PMC21Bglde1 KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

PMC21C1C5 KGENGSSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

C5

351 400

H41 SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVGDALNVN QLQNSGWNLD

PMC21 SGTNVTFASG KGTTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD

H41Studel SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVGDALNVN QLQNSGWNLD

PMC21Bglde1 SGTNVTFASG KGTTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD

PMC21C1C5 SGTNVTFASG KGTTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD

C5

FIG. 10

401 450
H41 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
H41Studel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21Bgldel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
PMC21C1C5 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM
C5

451 500
H41 TPQFSSVSLG AGADAPTLVS DDEGALNVGS KDANKPVRII NVAPGVKEGD
PMC21 TPQFSSVSLG AGADAPTLVS DG.DALNVGS KKDNKPVRII NVAPGVKEGD
H41Studel TPQFSSVSLG AGADAPTLVS DDEGALNVGS KDANKPVRII NVAPGVKEGD
PMC21Bgldel TPQFSSVSLG AGADAPTLVS DG.DALNVGS KKDNKPVRII NVAPGVKEGD
PMC21C1C5 TPQFSSVSLG AGADAPTLVS DG.DALNVGS KKDNKPVRII NVAPGVKEGD
C5

501 550
H41 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMMA
H41Studel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21Bgldel VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMMA
PMC21C1C5 VTNVAQLKGV AQNLNNRIDN VDGNNARAGIA QAIATAGLVQ AYLPGKSMMMA
C5

551 600
H41 IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
H41Studel IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYQW.
PMC21Bgldel IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
PMC21C1C5 IGGGTYRGEA GYAIGYSSIS DGGNWIIGKT ASGNSRGHFG ASASVGYQW.
C5

FIG. 10 cont'd

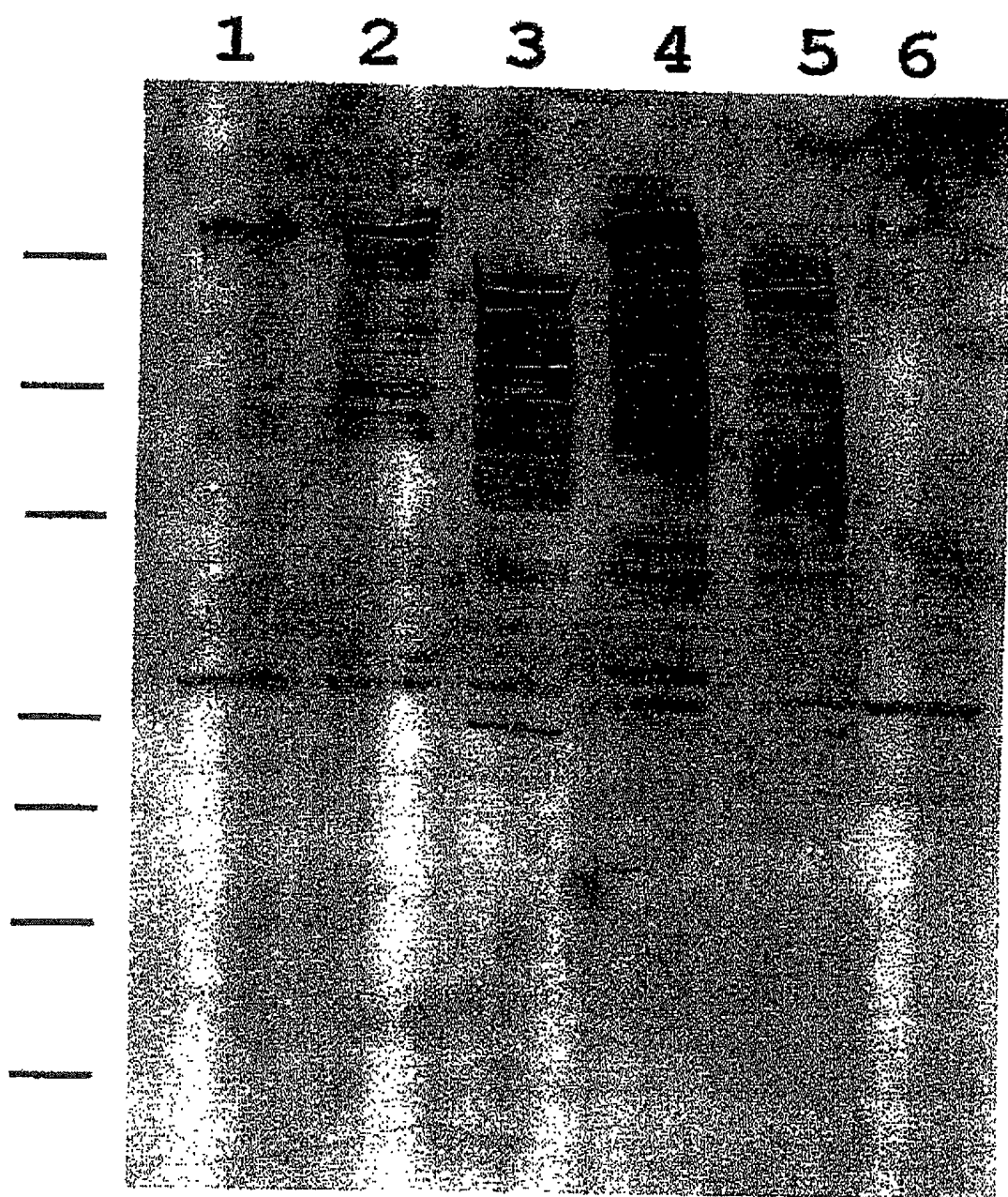


FIG. 11

1 2 3 4 5 6 7

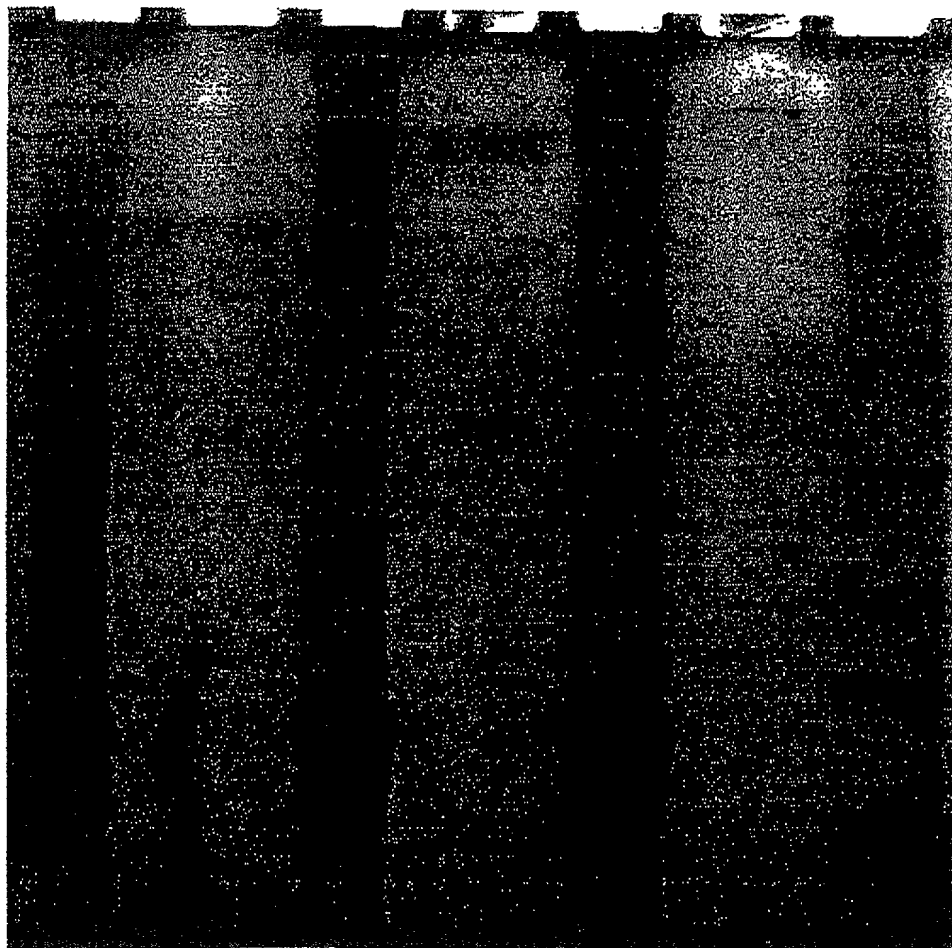
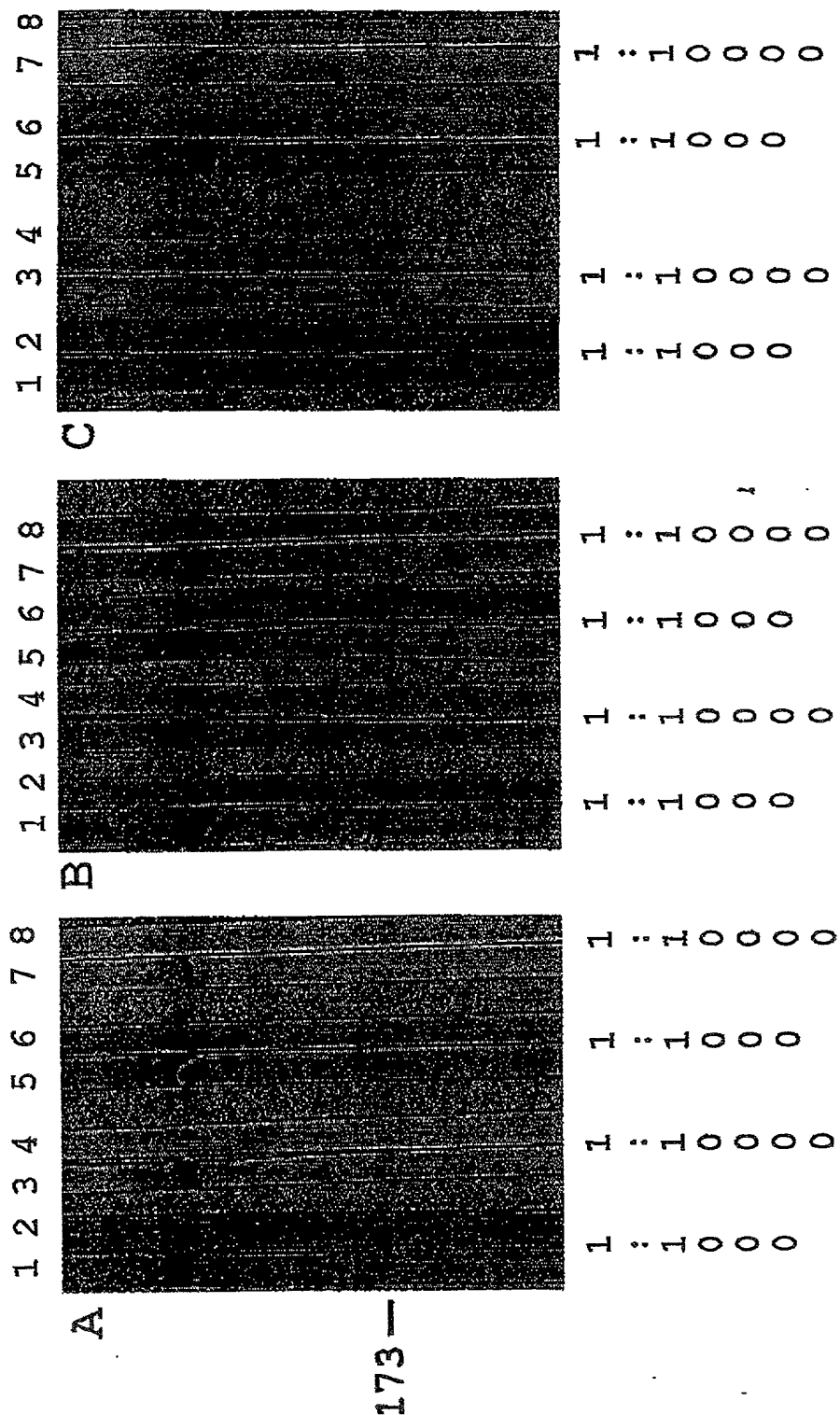


FIG. 12



A

52 NNEEQEEYL YLHPVQRTVA VLVNSDKEG AGEKEKVEEN SDWAVYFNEK
101 GVLTAAREITL KAGDNLKIKQ NGTNFTYSLK KDLTDLTSVG TEKLSFSAHG
151 NKVNITSDDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDTL LNTGATTNVT
201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL
251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS
301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF
351 ASGKGTTATV SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
401 SGKVISGNVS PSKGKMDTV NINAGNNIEI TRNGKNIDIA TSMTPOFSSV
451 SLGAGADAPT LSVGDALNV GSKKDNKPVR ITNVAPGVKE GDVTNVAQLK
501 GVAQNLNNRI DNVDGNARAG IAQAIATAGL VQAYLPGKSM MAIGGGTYRG
551 EAGYAIGYSS ISDGGNWIIG GTASGNSRGH FGASASVGYQ W*

B

52 TDEDEEEEL ESQRSVVGS IQASMEGSVE LETISLSMTN DSKEFVDPYI
101 VVTLKAGDNL KIKQNTNENT NASSFTYSLK KDLTG LINVE TEKLSFGANG
151 KKVNIISDDTK GLNFAKETAG TNGDTTVHLN GIGSTLTDM LNTGATTNVT
201 NDNVTDDEKK RAASVKDVLN AGWNIKGVPK GTTASDNVDF VRTYDTVEFL
251 SADTKTTTVN VESKDNGKKT EVKIGAKTSV IKEKDGLVT GKDKGENGSS
301 TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTKVTF
351 ASGNGTTATV SKDDQGNITV KYDVNVGDAL NVNQLQNSGW NLDSKAVAGS
401 SGKVISGNVS PSKGKMDTV NINAGNNIEI TRNGKNIDIA TSMTPOFSSV
451 SLGAGADAPT LSVDDGALN VSGKDANKPV RITNVAPGVK EGDVTNVAQL
501 KGVAQNLNNR IDNVNGNARA GIAQAIATAG LVQAYLPGKS MMAIGGGTYL
551 GEAGYAIGYS SISAGGNWII KGTASGNSRG HFGASASVGY QW*

FIG. 14

C

52 NNETDLTSV GTEKLSFSAN GNKVNITS DT KGLNFAKETA GTNGD TTVHL
 101 NGIGSTLTDT LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEDGKLV TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
 251 NGQTGQADKF ETVTSGTNVT FASGKGTTAT VSKDDQGNIT VMYDVNVGDA
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV
 401 RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG
 451 LVQAYLPGKS MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG
 501 HFGASASVGY QW*

D

52 TDETGLINV ETEKLSFGAN GKKVNIISDT KGLNFAKETA GTNGD TTVHL
 101 NGIGSTLTDM LLNTGATTNV TNDNVT DDEK KRAASVKDVL NAGWNIKGVK
 151 PGTTASDNVD FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS
 201 VIKEDGKLV TGKKGGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTTA
 251 NGQTGQADKF ETVTSGTKVT FASGNGTTAT VSKDDQGNIT VKYDVNVGDA
 301 LNVNQLQNSG WNLDKAVAG SSGKVISGNV SPSKGKMD ET VNINAGNNIE
 351 ITRNGKNIDI ATSMTPQFSS VSLGAGADAP TLSVDDEGAL NVGSKDANKP
 401 VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN RIDNVNGNAR AGIAQAIATA
 451 GLVQAYLPGK SMMAIGGGTY LGEAGYAIGY SSISAGGNWI IKGTASGNSR
 501 GHFGASASVG YQW*

FIG. 14

E

52 NNVDFVRTY DTVEFLSADT KTTTVNVESK DNGKKTEVKI GAKTSVIKEK
101 DGKLVTKGDK GENGSSTDEG EGLVTAKEVI DAVNKAGWRM KTTTANGQTG
151 QADKFETVTS GTNVTFASGK GTTATVSKDD QGNITVMYDV NVGDALNVNQ
201 LQNSGWNLDS KAVAGSSGKV ISGNVSPSKG KMDETVMNINA GNNIEITRNG
251 KNIDIATSMT PQFSSVSLGA GADAPTLSVD GDALNVGSKK DNKPVRITNV
301 APGVKEGDTV NVAQLKGVAQ NLNNRIDNVD GNARAGIAQA IATAGLVQAY
351 LPGKSMMMAIG GGTyrGEAGY AIGYSSISDG GNWIIKGTAS GNSRGHFGAS
401 ASVGYQW*

F

52 NRAASVKDV LNAGWNIKGV KPGTTASDNV DFVRTYDTVE FLSADTKTTT
101 VNVESKDNGK KTEVKIGAKT SVIKEKDGKL VTGKDKGENG SSTDEGEGLV
151 TAKEVIDAVN KAGWRMKTTH ANGQTGQADK FETVTSMTNV TFASGKGTTA
201 TVSKDDQGNITVMYDVNVGD ALNVNQLQNS GWNLDSKAVA GSSGKVISGN
251 VSPSKGKMDE TVNINAGNNI EITRNGKNID IATSMTPQFS SVSLGAGADA
301 PTLSDVDGAL NVGSKKDNKP VRITNVAPGV KEGDVTNVAQ LKGVAQNLNN
351 RIDNVDGNAR AGIAQAIATA GLVQAYLPGK SMAIGGGTY RGEAGYAIGY
401 SSISDGGNWI IKGTASGNSR GHFGASASVG YQW*

G

50 SANTLKAGDNL KIKQFTYSLK KDLTDLTSVG TEKLSFSANG NKVNITSDTK
101 GLNFAKETAG TNGDTTVHLN GIGSTLTDRA ASVKDVLNAG WNIKGVKNVD
151 FVRTYDTVEF LSADTKTTTV NVESKDNGKK TEVKIGAKTS VIKKDGKLV
201 TGKDKGENGS STDEGEGLVT AKEVIDAVNK AGWRMKTTHA NGQTGQADKF
251 ETVTSMTNVTFASGKGTAT VSKDDQGNITVMYDVNVGDA LNVNQLQNSG
301 WNLDKAVAG SSGKVISGNV SPSKGKMDET VNINAGNNIE ITRNGKNIDI
351 ATSMTPQFSS VSLGAGADAP TLSVDGDALN VGSKKDNKPV RITNVAPGVK
401 EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS
451 MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY
501 QW*

FIG. 14